RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/584,773
Source: IFWP
Date Processed by STIC: 6/14/06

ENTERED

IFWP

RAW SEQUENCE LISTING DATE: 06/14/2006
PATENT APPLICATION: **US/10/581,773** TIME: 10:14:31

Input Set : **A:\42100.txt**
Output Set: **N:\CRF4\06142006\J581773.raw**

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     4 <110> APPLICANT: Imperial College Innovations Limited
     6 <120> TITLE OF INVENTION: Therapeutically Useful Molecules
     8 <130> FILE REFERENCE: 28646/42100
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/581,773
C--> 11 <141> CURRENT FILING DATE: 2006-06-06
    13 <150> PRIOR APPLICATION NUMBER: GB 0328363.7
    14 <151> PRIOR FILING DATE: 2003-12-06
    16 <160> NUMBER OF SEQ ID NOS: 18
    18 <170> SOFTWARE: SeqWin99
    20 <210> SEQ ID NO: 1
    21 <211> LENGTH: 9
    22 <212> TYPE: PRT
    23 <213> ORGANISM: Artificial Sequence
    25 <220> FEATURE:
    26 <223> OTHER INFORMATION: Peptide of WT1 which is presented by HLA-A2 class I molecules
    28 <400> SEQUENCE: 1
    29 Arg Met Phe Pro Asn Ala Pro Tyr Leu
    30 1               5
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    33 <211> LENGTH: 6
    34 <212> TYPE: PRT
    35 <213> ORGANISM: Artificial Sequence
    37 <220> FEATURE:
    38 <223> OTHER INFORMATION: CDR1 of human TCR V -1.5 (V -8.2)
    40 <400> SEQUENCE: 2
    41 Ser Ser Tyr Ser Pro Ser
    42 1               5
    44 <210> SEQ ID NO: 3
    45 <211> LENGTH: 7
    46 <212> TYPE: PRT
    47 <213> ORGANISM: Artificial Sequence
    49 <220> FEATURE:
    50 <223> OTHER INFORMATION: CDR2 of human TCR V -1.5 (V -8.2)
    52 <400> SEQUENCE: 3
    53 Tyr Thr Ser Ala Ala Thr Leu
    54 1               5
    56 <210> SEQ ID NO: 4
    57 <211> LENGTH: 14
    58 <212> TYPE: PRT
    59 <213> ORGANISM: Artificial Sequence
    61 <220> FEATURE:
    62 <223> OTHER INFORMATION: CDR3 of human TCR V -1.5 (V -8.2) - 1
    64 <400> SEQUENCE: 4
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PATENT APPLICATION: **US/10/581,773** TIME: 10:14:31

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66 1               5                   10
68 <210> SEQ ID NO: 5
69 <211> LENGTH: 12
70 <212> TYPE: PRT
71 <213> ORGANISM: Artificial Sequence
73 <220> FEATURE:
74 <223> OTHER INFORMATION: CDR3 of human TCR V -1.5 (V -8.2) - 2
76 <400> SEQUENCE: 5
77 Ser Pro Phe Ser Gly Gly Gly Ala Asp Gly Leu Thr
78 1               5                   10
80 <210> SEQ ID NO: 6
81 <211> LENGTH: 6
82 <212> TYPE: PRT
83 <213> ORGANISM: Artificial Sequence
85 <220> FEATURE:
86 <223> OTHER INFORMATION: CDR1 of human TCR V -2.1 (V -20.1)
88 <400> SEQUENCE: 6
89 Asp Phe Gln Ala Thr Thr
90 1               5
92 <210> SEQ ID NO: 7
93 <211> LENGTH: 7
94 <212> TYPE: PRT
95 <213> ORGANISM: Artificial Sequence
97 <220> FEATURE:
98 <223> OTHER INFORMATION: CDR2 of human TCR V -2.1 (V -20.1)
100 <400> SEQUENCE: 7
101 Ser Asn Glu Gly Ser Lys Ala
102 1               5
104 <210> SEQ ID NO: 8
105 <211> LENGTH: 8
106 <212> TYPE: PRT
107 <213> ORGANISM: Artificial Sequence
109 <220> FEATURE:
110 <223> OTHER INFORMATION: CDR3 of human TCR V -2.1 (V -20.1) - 1
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113 Ser Ala Arg Asp Gly Gly Glu Gly
114 1               5
116 <210> SEQ ID NO: 9
117 <211> LENGTH: 11
118 <212> TYPE: PRT
119 <213> ORGANISM: Artificial Sequence
121 <220> FEATURE:
122 <223> OTHER INFORMATION: CDR3 of human TCR V -2.1 (V -20.1) - 2
124 <400> SEQUENCE: 9
125 Arg Asp Gly Gly Glu Gly Ser Glu Thr Gln Tyr
126 1               5                   10
128 <210> SEQ ID NO: 10
129 <211> LENGTH: 11
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RAW SEQUENCE LISTING DATE: 06/14/2006
PATENT APPLICATION: **US/10/581,773** TIME: 10:14:31

Input Set : **A:\42100.txt**
Output Set: **N:\CRF4\06142006\J581773.raw**

130 <212> TYPE: PRT
131 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: Framework amino acid sequence of constant portion C-terminal to
135 CDR3
137 <400> SEQUENCE: 10
138 Phe Gly Lys Gly Thr His Leu Ile Ile Gln Pro
139 1 5 10
141 <210> SEQ ID NO: 11
142 <211> LENGTH: 5
143 <212> TYPE: PRT
144 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
147 <223> OTHER INFORMATION: Beginning of constant region of human TCR V -1.5 (V -8.2)
149 <400> SEQUENCE: 11
150 Tyr Ile Gln Asn Pro
151 1 5
153 <210> SEQ ID NO: 12
154 <211> LENGTH: 5
155 <212> TYPE: PRT
156 <213> ORGANISM: Artificial Sequence
158 <220> FEATURE:
159 <223> OTHER INFORMATION: Beginning of framework amino acid sequence of human TCR V -2.1 (V
160 -20.1)
162 <400> SEQUENCE: 12
163 Ser Glu Thr Gln Tyr
164 1 5
166 <210> SEQ ID NO: 13
167 <211> LENGTH: 10
168 <212> TYPE: PRT
169 <213> ORGANISM: Artificial Sequence
171 <220> FEATURE:
172 <223> OTHER INFORMATION: Part of framework amino acid sequence of human TCR V -2.1 (V -20.1)
174 <400> SEQUENCE: 13
175 Phe Gly Pro Gly Thr Arg Leu Leu Val Leu
176 1 5 10
178 <210> SEQ ID NO: 14
179 <211> LENGTH: 5
180 <212> TYPE: PRT
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Part of constant region of human TCR V -2.1 (V -20.1)
186 <400> SEQUENCE: 14
187 Glu Asp Leu Lys Asn
188 1 5
190 <210> SEQ ID NO: 15
191 <211> LENGTH: 830
192 <212> TYPE: DNA
193 <213> ORGANISM: Human TCR V -1.5 (V -8.2)

RAW SEQUENCE LISTING DATE: 06/14/2006
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Input Set : **A:\42100.txt**
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195 <400> SEQUENCE: 15
196 atgctcctgc tgctcgtccc agtgctcgag gtgattttta ctctgggagg aaccagagcc 60
197 cagtcggtga cccagcttga cagccacgtc tctgtctctg aaggaacccc ggtgctgctg 120
198 aggtgcaact actcatcttc ttattcacca tctctcttct ggtatgtgca acaccccaac 180
199 aaaggactcc agcttctcct gaagtacaca tcagcggcca ccctggttaa aggcatcaac 240
200 ggttttgagg ctgaatttaa gaagagtgaa acctccttcc acctgacgaa accctcagcc 300
201 catatgagcg acgcggctga gtacttctgt gttgtgagtc ctttttcagg aggaggtgct 360
202 gacggactca cctttggcaa agggactcat ctaatcatcc agccctatat ccagaaccct 420
203 gaccctgccg tgtaccagct gagagactct aaatccagtg acaagtctgt ctgcctattc 480
204 accgattttg attctcaaac aaatgtgtca caaagtaagg attctgatgt gtatatcaca 540
205 gacaaaactg tgctagacat gaggtctatg gacttcaaga gcaacagtgc tgtggcctgg 600
206 agcaacaaat ctgactttgc atgtgcaaac gccttcaaca acagcattat tccagaagac 660
207 accttcttcc ccagcccaga aagttcctgt gatgtcaagc tggtcgagaa aagctttgaa 720
208 acagatacga acctaaactt tcaaaacctg tcagtgattg ggttccgaat cctcctcctg 780
209 aaagtggccg ggtttaatct gctcatgacg ctgcggctgt ggtccagctg 830
211 <210> SEQ ID NO: 16
212 <211> LENGTH: 276
213 <212> TYPE: PRT
214 <213> ORGANISM: Human TCR V -1.5 (V -8.2)
216 <400> SEQUENCE: 16
217 Met Leu Leu Leu Leu Val Pro Val Leu Glu Val Ile Phe Thr Leu Gly
218 1 5 10 15
220 Gly Thr Arg Ala Gln Ser Val Thr Gln Leu Asp Ser His Val Ser Val
221 20 25 30
223 Ser Glu Gly Thr Pro Val Leu Leu Arg Cys Asn Tyr Ser Ser Ser Tyr
224 35 40 45
226 Ser Pro Ser Leu Phe Trp Tyr Val Gln His Pro Asn Lys Gly Leu Gln
227 50 55 60
229 Leu Leu Leu Lys Tyr Thr Ser Ala Ala Thr Leu Val Lys Gly Ile Asn
230 65 70 75 80
232 Gly Phe Glu Ala Glu Phe Lys Lys Ser Glu Thr Ser Phe His Leu Thr
233 85 90 95
235 Lys Pro Ser Ala His Met Ser Asp Ala Ala Glu Tyr Phe Cys Val Val
236 100 105 110
238 Ser Pro Phe Ser Gly Gly Gly Ala Asp Gly Leu Thr Phe Gly Lys Gly
239 115 120 125
241 Thr His Leu Ile Ile Gln Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val
242 130 135 140
244 Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe
245 145 150 155 160
247 Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp
248 165 170 175
250 Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe
251 180 185 190
253 Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys
254 195 200 205
256 Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro
257 210 215 220
259 Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu

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Output Set: **N:\CRF4\06142006\J581773.raw**

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260 225                 230                 235                 240
262 Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg
263                 245                 250                 255
265 Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg
266             260                 265                 270
268 Leu Trp Ser Ser
269         275
271 <210> SEQ ID NO: 17
272 <211> LENGTH: 933
273 <212> TYPE: DNA
274 <213> ORGANISM: Human TCR V -2.1 (V -20.1)
276 <400> SEQUENCE: 17
277 atgctgctgc ttctgctgct tctggggcca ggctccgggc ttggtgctgt cgtctctcaa   60
278 catccgagct gggttatctg taagagtgga acctctgtga agatcgagtg ccgttccctg   120
279 gactttcagg ccacaactat gttttggtat cgtcagttcc cgaaacagag tctcatgctg   180
280 atggcaactt ccaatgaggg ctccaaggcc acatacgagc aaggcgtcga gaaggacaag   240
281 tttctcatca accatgcaag cctgaccttg tccactctga cagtgaccag tgcccatcct   300
282 gaagacagca gcttctacat ctgcagtgct agagatgggg gggagggttc ggagacccag   360
283 bgcttcgggc cagggcacgcg gctcctggtg ctcgaggacc tgaaaaacgt gttcccaccc   420
284 gaggtcgctg tgtttgagcc atcagaagca gagatctccc acacccaaaa ggccacactg   480
285 gtgtgcctgg ccacaggctt ctaccccgac cacgtggagc tgagctggtg ggtgaatggg   540
286 aaggaggtgc acagtggggt cagcacagac ccgcagcccc tcaaggagca gcccgccctc   600
287 aatgactcca gatactgcct gagcagccgc ctgagggtct cggccacctt ctggcagaac   660
288 ccccgcaacc acttccgctg tcaagtccag ttctacgggc tctcggagaa tgacgagtgg   720
289 acccaggata gggccaaacc tgtcacccag atcgtcagcg ccgaggcctg gggtagagca   780
290 gactgtggct tcacctccga gtcttaccag caaggggtcc tgtctgccac catcctctat   840
291 gagatcttgc tagggaaggc caccttgtat gccgtgctgg tcagtgccct cgtgctgatg   900
292 gccatggtca agagaaagga ttccagaggc tag                               933
294 <210> SEQ ID NO: 18
295 <211> LENGTH: 310
296 <212> TYPE: PRT
297 <213> ORGANISM: Human TCR V -2.1 (V -20.1)
299 <400> SEQUENCE: 18
300 Met Leu Leu Leu Leu Leu Leu Leu Gly Pro Gly Ser Gly Leu Gly Ala
301 1               5                   10                  15
303 Val Val Ser Gln His Pro Ser Trp Val Ile Cys Lys Ser Gly Thr Ser
304             20                  25                  30
306 Val Lys Ile Glu Cys Arg Ser Leu Asp Phe Gln Ala Thr Thr Met Phe
307         35                  40                  45
309 Trp Tyr Arg Gln Phe Pro Lys Gln Ser Leu Met Leu Met Ala Thr Ser
310     50                  55                  60
312 Asn Glu Gly Ser Lys Ala Thr Tyr Glu Gln Gly Val Glu Lys Asp Lys
313 65                  70                  75                  80
315 Phe Leu Ile Asn His Ala Ser Leu Thr Leu Ser Thr Leu Thr Val Thr
316                 85                  90                  95
318 Ser Ala His Pro Glu Asp Ser Ser Phe Tyr Ile Cys Ser Ala Arg Asp
319             100                 105                 110
321 Gly Gly Glu Gly Ser Glu Thr Gln Tyr Phe Gly Pro Gly Thr Arg Leu
322         115                 120                 125
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VERIFICATION SUMMARY DATE: 06/14/2006
PATENT APPLICATION: **US/10/581,773** TIME: 10:14:32

Input Set : **A:\42100.txt**
Output Set: **N:\CRF4\06142006\J581773.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date